



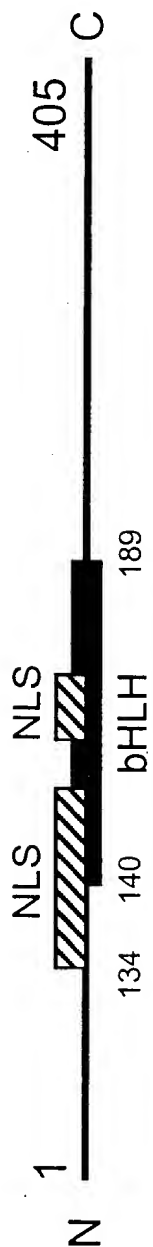
Title: PHELIX: A TESTIS-SPECIFIC PROTEIN EXPRESSED IN  
CANCER

First Inventor: Daniel E. H. AFAR, *et al.*

Application No.: 09/389,000

Docket No.: 511582002700

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NLS = nuclear localization signals, residues 134-150, 163-169.  
bHLH = basic helix-loop-helix domain, residues 140-189.

FIG. 1



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5' 11 20 29 38 47 56  
GAC CGG GGG GCG GTT GGG GTT CAC CGC CTC GTG CCG TAC TGG CTT CTG GGT GGC  
-----  
65 74 83 92 101 110  
CCT TAA TGT CTT GTG CTC TAA GGT GCT GAG GGG AAA GAC GCG GGA GGT CTC TGG  
-----  
119 128 137 146 155 164  
CCT GAC ACT ATG AAG GAA GAG AGA AAC TAC AAC TTC GAC GGT GTG AGC ACC AAC  
-----  
173 182 191 200 209 218  
CGC CTG AAA CAG CAG TTG CTG GAA GAA GTC CGC AAG AAG TAG TGA ATG GAA AAC  
-----  
227 236 245 254 263 272  
CCG TTA TGA GAC ACA ACT TGA ATT AAA TGA TGA ACT AGA AAA GCA AAT TGT TTA  
-----  
281 290 299 308 317 326  
TCT CAA GGA GAA AGT GGA AAA AAT CCA TGG AAA CTC TTC AGA TAG ACT ATC TTC  
-----  
335 344 353 362 371 380  
TAT TCG TGT CTA TGA ACG AAT GCC AGT GGA ATC CTT AAA CAC ATT ACT TAA ACA  
-----  
389 398 407 416 425 434  
GCT AGA AGA AGA AAA GAA GAC TCT TGA AAG TCA AGT GAA ATA CTA TGC ACT TAA  
-----  
443 452 461 470 479 488  
ACT GGA ACA AGA ATC AAA GGC TTA CCA GAA GAT CAA CAA TGA ACG CCG TAC ATA  
-----  
497 506 515 524 533 542  
CCT AGC TGA AAT GTC TCA GGG TTC TGG TTT ACA TCA AGT TTC TAA AAG GCA ACA  
-----  
551 560 569 578 587 596  
GGT GGA TCA ACT GCC TAG GAT GCA AGA GAA TCT AGT GAA AAC GCA AAA ATA GAC  
-----  
605 614 623 632 641 650  
ATC TTA TTA GTT GGA GAT GTC ACT GTG GGC TAC CTG GCT GAT ACT GTA CAG AAA  
-----  
659 668 677 686 695 704  
CTA TTT GCA AAC ATA GCA GAA GTC ACC ATC ACC ATC AGT GAC ACG AAG GAG GCA  
-----  
713 722 731 740 749 758  
GCA GCG CTT TTG GAT GAT TGC ATA TTC AAC ATG GTT CTC TTG AAG GTG CCT TCT  
-----  
M V L L K V P S  
-----  
767 776 785 794 803 812  
TCA CTA AGT GCC GAG GAG CTG GAA GCC ATC AAG TTA ATT AGA TTT GGC AAA AAG  
-----  
S L S A E E L E A I K L I R F G K K  
-----  
821 830 839 848 857 866  
AAA AAT ACA CAT TCA CTG TTT GTT TTT ATA ATC CCT GAA AAT TTT AAA GGT TGT  
-----  
K N T H S L F V F I I P E N F K G C  
-----  
875 884 893 902 911 920  
ATT TCA GGG CAT GGA ATG GAT ATT GCT TTA ACT GAA CCA CTG ACA ATG GAA AAA  
-----  
I S G H G M D I A L T E P L T M E K  
-----  
929 938 947 956 965 974  
ATG AGT AAT GTG GTA AAA TAC TGG ACA ACA TGT CCC TCA AAC ACT GTT AAG ACT  
-----  
M S N V V K Y W T T C P S N T V K T

FIG. 2A



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983	992	1001	1010	1019	1028
GAA AAC GCA ACT GGG CCT GAA GAA CTT GGA TTG CCC CTG CAG AGG TCC TAC AGC					
E N A T G P E E L G L P L Q R S Y S					
1037	1046	1055	1064	1073	1082
GAA CAC CTG GGA TAT TTT CCT ACT GAT CTA TTT GCC TGC TCT GAA TCT TTA AGG					
E H L G Y F P T D L F A C S E S L R					
1091	1100	1109	1118	1127	1136
AAT GGC AAT GGG CTT GAA TTA AAT GCT TCG TTG TCA GAG TTC GAG AAA AAC AAA					
N G N G L E L N A S L S E F E K N					
1145	1154	1163	1172	1181	1190
AAG ATC TCT CTT CTT CAT TCA AGC AAG GAA AAA CTA AGA AGG GAA AGA ATC AAA					
K I S L L R S S K E K L R R E R I K					
1199	1208	1217	1226	1235	1244
TAT TGC TGT GAG CAG CTG CGT ACT CTC TTG CCG TAT GTA AAA GGG AGA AAG AAT					
Y C C E Q L R T L L F Y V K G R K N					
1253	1262	1271	1280	1289	1298
GAT GCG GCT TCA GTT CTT GAG GCA ACA GTT GAT TAT GTG AAA TAT ATC CGG GAG					
D A A S V L E A T V D Y V K Y I R E					
1307	1316	1325	1334	1343	1352
AAA ATC TCT CCA GCC GTT ATG GCC CAG ATT ACA GAA GCA CTT CAG AGC AAC ATG					
K I S P A V M A Q I T E A L Q S N M					
1361	1370	1379	1388	1397	1406
AGG TTT TGT AAG AAA CAA CAA ACA CCC ATT GAG CTG TCT CTC CCA GGC ACT GTC					
R F C K K Q Q T P I E L S L P G T V					
1415	1424	1433	1442	1451	1460
ATG GCA CAG CGG GAA AAC AGT GTG ATG AGC ACT TAC TCC CCT GAG AGA GGG CTC					
M A Q R E N S V M S T Y S P E R G L					
1469	1478	1487	1496	1505	1514
CAA TTC CTG ACT AAT ACG TGC TGG AAT GGG TGC TCC ACT CCT GAT GCA GAG AGC					
Q F L T N T C W N G C S T P D A E S					
1523	1532	1541	1550	1559	1568
TCC TTG GAT GAA GCT GTG AGA GTT CCA TCA AGC TCC GCC TCA GAG AAT GCT ATT					
S L D E A V R V P S S S A S E N A I					
1577	1586	1595	1604	1613	1622
GGT GAT CCA TAT AAA ACT CAC ATT TCC AGT GCA GCG CTG TCT CTG AAT TCC TTG					
G D P Y K T H I S S A A L S L N S L					
1631	1640	1649	1658	1667	1676
CAT ACT GTC AGA TAT TAT TCT AAA GTC ACC CCT TCC TAC GAT GCA ACT GCT GTA					
H T V R Y Y S K V T P S Y D A T A V					

FIG. 2B



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1685      1694      1703      1712      1721      1730
ACA AAT CAG AAC ATT TCA ATT CAT TTA CCT TCA GCC ATG CCC CCG GTC TCA AGC
-----
T   N   Q   N   I   S   I   H   L   P   S   A   M   P   P   V   S   S

1739      1748      1757      1766      1775      1784
TTC TCC CTC GGC ACT GCA CTT CTG GGT TGG GCC AGA CGT GCA CTA CAC ATC CCA
-----
F   S   L   G   T   A   L   L   G   W   A   R   R   A   L   H   I   P

1793      1802      1811      1820      1829      1838
ACT GTC TGC AAC AGT TTT GGG CGT ATT AAA AGC ACA TGT TTG AAA TTC ACA CTC
-----
T   V   C   N   S   F   G   R   I   K   S   T   C   L   K   F   T   L

1847      1856      1865      1874      1883      1892
TCA ACC ACC TAC TGG GCG CAG TTT GAC AAT CTA GGA AAA GTG GAA CAA AGA ATG
-----
S   T   T   Y   W   A   Q   F   D   N   L   G   K   V   E   Q   R   M

1901      1910      1919      1928      1937      1946
ATT TTG AAA GCT CCA CCC AAA GAC CTA ATA TCA AAA GAG TTG GCA TGG TTT GGC
-----
I   L   K   A   P   P   K   D   L   I   S   K   E   L   A   W   F   G

1955      1964      1973      1982      1991      2000
TTC TGA TAA ATG CAC TCA AAG CTT CTG CAG ATA GAA AGA CCA GCA GCG AAA AAG
-----
F   *   *

2009      2018      2027      2036      2045      2054
CTG GCC ACA CAC TGT CAC TCA TCT TCA TAC ACA CTT GGA TCC CCG CCA GCC AGA
-----
2063      2072      2081      2090      2099      2108
GAG CTA CAA GAA CAA ATG GCC TCA GTG ACC TAC ACT CTC TTT TCT CAA AAA ATA
-----
2117      2126
TTC CAC AAT TTA TGA AAA AAA A 3'
-----
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FIG. 2C



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Homology with Max (rat)

gnl|PID|d1003848 (D14448) Max [Rattus norvegicus]  
Length = 151

Score = 93 (42.1 bits), Expect = 0.00037, P = 0.00037  
Identities = 17/50 (34%), Positives = 30/50 (60%)

22P4G9: 5 HSSKEKLRRERIKYCCEQLRTLTPYVKGRKNDAAVLEATVDYVKYIREK 54  
H++ E+ RR+ IK LR +P ++G K A +L+ +Y++Y+R K  
Max: 19 HNALERKRRDHIKDSFHSRLRDSVPSLQGEKASRAQILDKATEYIQYMRRK 68

Homology with Mxi (zebrafish)

sp|P50541|MXI1\_BRARE MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN)  
gi|505977  
(U10638) zMxi1 [Brachydanio rerio]  
Length = 243

Score = 64 (29.0 bits), Expect = 3.3, P = 0.96  
Identities = 11/24 (45%), Positives = 17/24 (70%)

22P4G9: 5 HSSKEKLRRERIKYCCEQLRTLTP 28  
H+ EK RR ++ C E+L+TL+P  
Mxi: 81 HNELEKNRRRAHLRLCLERLKTLP 104

FIG. 3